

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2006, 13:20:45 ; Search time 16567.7 Seconds
(without alignments)
10189.779 Million cell updates/sec

Title: US-10-767-441-9
Perfect score: 2640
Sequence: 1 taaacggcgataataaata.....acaggattaattcccgacc 2640

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues
Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb env.*
- 2: gb pat.*
- 3: gb ph.*
- 4: gb pl.*
- 5: gb pr.*
- 6: gb ro.*
- 7: gb sts.*
- 8: gb sy.*
- 9: gb un.*
- 10: gb vi.*
- 11: gb ov.*
- 12: gb htg.*
- 13: gb in.*
- 14: gb om.*
- 15: gb ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2640	100.0	225528	15	AL591984 Listeria
2	2640	100.0	244528	2	AX641673 Sequence
3	2556	96.8	2556	2	AX413703 Sequence
4	2556	96.8	2556	2	AX415879 Sequence
5	2197.6	83.2	105187	15	Continuation (29 o
6	977.4	37.0	3318	2	AX416769 Sequence
7	676.2	25.6	759	2	AX415918 Sequence
8	530.4	20.1	3084	2	AX416693 Sequence
9	269.2	10.2	110000	15	AX414526 Sequence
10	269.2	10.2	110000	15	Continuation (9 of
11	232	8.8	260050	15	AL596166 Listeria
12	232	8.8	349980	2	AX417039 Sequence
13	232	8.8	349980	2	AX417042 Sequence
14	231	8.8	1941	2	AX413668 Sequence
15	231	8.8	1974	2	AX415259 Sequence
16	224	8.5	3714	2	AX415307 Sequence
17	224	8.5	3735	2	AX413690 Sequence
18	224	8.5	263020	2	AX417040 Sequence

19	224	8.5	333050	15	AL596168
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24	204.2	7.7	324050	15	AL591983 Listeria
25	204.2	7.7	349980	2	AX641672 Sequence
26	202.8	7.7	110000	15	Continuation (25 o
27	199.8	7.6	224650	15	AL596164 Listeria
28	199.8	7.6	349980	2	AX417041 Sequence
29	199.8	7.6	349980	2	AX453571 Sequence
30	191.6	7.3	248050	15	AL596172 Listeria
31	191.6	7.3	349980	2	AX413018 Sequence
32	191.6	7.3	349980	2	AX417048 Sequence
33	188	7.1	160050	15	AL591974 Listeria
34	188	7.1	349980	2	AX641665 Sequence
35	186.8	7.1	2977	2	AX416727 Sequence
36	185	7.0	849	2	AX416268 Sequence
37	183.2	6.9	110000	15	Continuation (4 of
38	177.4	6.7	1018	2	AX416178 Sequence
39	176.8	6.7	753	2	AX414618 Sequence
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42	140.2	5.3	895	2	AX414851 Sequence
43	138	5.2	1320	2	AX413786 Sequence
44	138	5.2	1320	2	AX415814 Sequence
45	138	5.2	240050	15	AL591979 Listeria

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
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ACCESSION
AL591984.1 GI:16412145
VERSION
AL591984.1
KEYWORDS
Listeria monocytogenes
SOURCE
Listeria monocytogenes
ORGANISM
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
REFERENCE
1.
AUTHORS
Glaser, P., Frangeul, L., Buchrieser, C., Rusniok, C., Amend, A., Baquero, F., Berche, P., Bloeker, H., Brandt, P., Chakraborty, T., Charbit, A., Chetoui, F., Couve, E., de Daruvar, A., Dehoux, F., Domann, S., Dominguez-Bernal, G., Duchaud, E., Durant, L., Dussurget, O., Entian, K.D., Fsihi, H., Garcia-del Portillo, F., Garrido, P., Gautier, L., Goebel, W., Gomez-Lopez, N., Hain, T., Hauf, J., Jackson, D., Jones, L.M., Kaerst, U., Kref, J., Kuhn, M., Kunst, F., Kurapkat, G., Madueno, E., Maitournam, A., Vicente, J.M., Ng, E., Nedjar, H., Nordstiek, G., Novella, S., de Pablo, B., Perez-Diaz, J.C., Purcell, R., Rammel, B., Rose, M., Schluter, T., Simoes, N., Tierrez, A., Vazquez-Boland, J.A., Voss, H., Wehland, J. and Cossart, P.

Comparative Genomics of Listeria species
Science 294 (5543), 849-852 (2001)
11679669
2 (bases 1 to 225528)
Glaser, P., Frangeul, L. and Rusniok, C.
Direct Submission
Submitted (06-JUN-2001) Glaser P., Institut Pasteur, Genomique des Microorganismes Pathogenes, 25 rue du Docteur Roux, 75724 Paris
Cedex 15, FRANCE
E-mail: pglaser@pasteur.fr
Phone: +33 1 45 68 89 96, Fax: +33 (0)1 45 68 87 86.
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gene

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RESULT 2
LOCUS AX641673 244528 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2863 from Patent WO0101118.
ACCESSION AX641673
VERSION AX641673.1 GI:28474434
KEYWORDS Listeria monocytogenes
SOURCE Listeria monocytogenes
ORGANISM Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
REFERENCE 1
AUTHORS Buchrieser,C., Frangeul,L., Couve,E., Rueniok,C., Pshhi,H., Dehoux,P., Dussurget,O., Chetouani,F., Nedjari,H., Glaser,P., Kunst,F., Cossart,P., Daniels,J., Goebel,W., Kreft,J., Kuhn,M., Ng,E., Vasquez-Boland,J., Dominguez-Bernal,G., Garrido-Garcia,P., Tierrez-Martinez,A., Amend,A., Chakraborty,T., Domann,E., Hain,T., Berche,P., Charbit,A., Durant,L., Perez-Diaz,J.C., Baquero,F., Garcia del Portillo,F., Gomez-Lopez,N., Madueno,E., de Fablos,B., Weiland,J., Kaerst,U., Entian,K.D., Hauf,J., Rose,M. and Voss,H.
TITLE Listeria monocytogenes genome, polypeptides and uses
JOURNAL Patent: WO 0101118-A 2863 11-APR-2001;
INSTITUT PASTEUR (FR)

FEATURES
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REFERENCE 1
AUTHORS Kunst, F. and Glaser, P.
TITLE Listeria innocua, genome and applications
JOURNAL Patent: WO 0228891-A 2870 11-APR-2002;
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RESULT 5

AE017262_28

WPCOMMENT

Sequence split into 29 fragments LOCUS AE017262 Accession AE017262

Fragment Name	Begin	End
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AE017262_02	200001	310000
AE017262_03	300001	410000
AE017262_04	400001	510000
AE017262_05	500001	610000
AE017262_06	600001	710000
AE017262_07	700001	810000
AE017262_08	800001	910000
AE017262_09	900001	1010000
AE017262_10	1000001	1110000
AE017262_11	1100001	1210000
AE017262_12	1200001	1310000
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AE017262_14	1400001	1510000
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AE017262_16	1600001	1710000
AE017262_17	1700001	1810000
AE017262_18	1800001	1910000
AE017262_19	1900001	2010000
AE017262_20	2000001	2110000
AE017262_21	2100001	2210000
AE017262_22	2200001	2310000
AE017262_23	2300001	2410000
AE017262_24	2400001	2510000
AE017262_25	2500001	2610000
AE017262_26	2600001	2710000
AE017262_27	2700001	2810000
AE017262_28	2800001	2905187

Continuation (29 of 29) of AE017262 from base 2800001 (AE017262 Listeria monocytogenes)

Query Match 83.2%; Score 2197.6; DB 15; Length 105187;
Best Local Similarity 88.1%; Pred. No. 0;
Matches 2511; Conservative 0; Mismatches 114; Indels 225; Gaps 2;

QY 1 TAAACCGCGGTATTAATAATGATTATAGAGAACGAATAGGAGTGCAGCAATTTGAAAAAC 60
DB 67562 TAAACCGCGGTATTAATAATGATTATAGAGAACGAATAGGAGTGCAGCAATTTGAAAAAC 67621
QY 61 TACTAAATAGTAAATTCCTCATTTAGTTTAAACCATGGTTTCAAAACCGCTTTTAAAC 120
DB 67622 TTCTAAATAATTAATAGTCTTCATTTAGTTTAAACCTGGTTTCAAAACCCCAATTTTAAAC 67681
QY 121 ATTGCGACCAAGCAATGATGTTTATGTATAATACGACAGAAATCACTACTGTATAAGAAAC 180
DB 67682 ATTGCGACCAAGCAATGATGTTTATGTATAGTACGACAGAAATCACTACTGTATAAGAAAT 67741
QY 181 AAGCTCAACTCAACCACTATAAAAAACACACTCAAGCCGTCACAAACAGTTTAA 240
DB 67742 AAGCTCAACTCAACCACTATAAAAAACCACTCAAGCTGGTCAAAACAGTTTAA 67801

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2006, 13:20:45 ; Search time 125.513 Seconds
(without alignments)
10189.779 Million cell updates/sec

Title: US-10-767-441-27

Perfect score: 20

Sequence: 1 ttacggctgattgtctgtg 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb_env.*
2: gb_pat.*
3: gb_ph.*
4: gb_pl.*
5: gb_pr.*
6: gb_ro.*
7: gb_ats.*
8: gb_sy.*
9: gb_un.*
10: gb_vi.*
11: gb_ov.*
12: gb_htg.*
13: gb_in.*
14: gb_om.*
15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	2556	2	AX413703 Sequence
C 2	20	100.0	2556	2	AX415879 Sequence
C 3	20	100.0	105187	15	AE017262_28 Continuation (29 o
C 4	20	100.0	225528	15	AL591984 Listeria
C 5	20	100.0	244528	2	AX641673 Sequence
C 6	19	95.0	125366	11	AX649277 Zebrafish
C 7	19	95.0	165089	11	AX649385 Zebrafish
C 8	19	95.0	222879	11	AX324175 Zebrafish
C 9	19	95.0	263011	12	AX914199 Danio rer
C 10	17.4	87.0	189351	12	AC156120 Bos tauru
C 11	17.4	87.0	189351	12	AC156120 Bos tauru
C 12	17.4	87.0	194849	12	AC147015 Zea mays
C 13	17.4	87.0	238338	12	AC162356 Bos tauru
C 14	17	85.0	110000	15	AE000512_13 Continuation (14 o
C 15	17	85.0	311522	12	AF235312 Bos tauru
C 16	16.8	84.0	183	7	AF235312 Sus scrof
C 17	16.8	84.0	1458	4	AF247136 Capsicum
C 18	16.8	84.0	89384	12	AP007333 Lotus cor

C 19	16.8	84.0	110000	4	AP007171_04 Continuation (5 of
C 20	16.8	84.0	110000	15	AP006627_29 Continuation (30 o
C 21	16.8	84.0	110000	15	BX950851_48 Continuation (49 o
C 22	16.8	84.0	112732	5	AL160007 Human DNA
C 23	16.8	84.0	113949	12	AC170863 Mus muscu
C 24	16.8	84.0	143794	5	AC009315 Homo sapi
C 25	16.8	84.0	148055	12	AC128178 Rattus no
C 26	16.8	84.0	167417	12	AC151166 Bos tauru
C 27	16.8	84.0	179038	12	AC171229 Bos tauru
C 28	16.8	84.0	182371	12	AC175370 Cavia por
C 29	16.8	84.0	185573	12	AC173137 Bos tauru
C 30	16.8	84.0	186522	12	AC169050 Bos tauru
C 31	16.8	84.0	194074	5	AC090095 Homo sapi
C 32	16.8	84.0	195446	6	AC133967 Mus muscu
C 33	16.8	84.0	195714	6	AC159208 Mus muscu
C 34	16.8	84.0	199810	5	AC018443 Homo sapi
C 35	16.8	84.0	208603	6	AC135567 Mus muscu
C 36	16.8	84.0	211158	6	AC123658 Mus muscu
C 37	16.8	84.0	222568	12	AC128034 Rattus no
C 38	16.8	84.0	231406	12	AC132626 Rattus no
C 39	16.8	84.0	238608	12	AC095637 Rattus no
C 40	16.8	84.0	243299	12	AC129672 Rattus no
C 41	16.8	84.0	245536	6	AC093320 Mus muscu
C 42	16.8	84.0	250502	12	AC098191 Rattus no
C 43	16.8	84.0	253762	12	AC094601 Rattus no
C 44	16.8	84.0	265323	12	AC095987 Rattus no
C 45	16.8	84.0	269126	12	AC096191 Rattus no

ALIGNMENTS

RESULT 1	AX413703/c	AX413703	Sequence	694	from Patent WO0228891.	2556 bp	DNA	linear	PAT 02-SEP-2002
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DEFINITION	AX413703	AX413703	AX413703	AX413703.1	GI:21446160				
ACCESSION	AX413703	AX413703	AX413703	AX413703.1	GI:21446160				
VERSION	AX413703.1	AX413703.1	AX413703.1	AX413703.1	GI:21446160				
KEYWORDS	AX413703.1	AX413703.1	AX413703.1	AX413703.1	GI:21446160				
SOURCE	AX413703.1	AX413703.1	AX413703.1	AX413703.1	GI:21446160				
ORGANISM	AX413703.1	AX413703.1	AX413703.1	AX413703.1	GI:21446160				
REFERENCE	AX413703.1	AX413703.1	AX413703.1	AX413703.1	GI:21446160				
AUTHORS	AX413703.1	AX413703.1	AX413703.1	AX413703.1	GI:21446160				
TITLE	AX413703.1	AX413703.1	AX413703.1	AX413703.1	GI:21446160				
JOURNAL	AX413703.1	AX413703.1	AX413703.1	AX413703.1	GI:21446160				
FEATURES	AX413703.1	AX413703.1	AX413703.1	AX413703.1	GI:21446160				
source	AX413703.1	AX413703.1	AX413703.1	AX413703.1	GI:21446160				
ORIGIN	AX413703.1	AX413703.1	AX413703.1	AX413703.1	GI:21446160				
Query Match	AX413703.1	AX413703.1	AX413703.1	AX413703.1	GI:21446160				
Best Local Similarity	AX413703.1	AX413703.1	AX413703.1	AX413703.1	GI:21446160				
Matches	AX413703.1	AX413703.1	AX413703.1	AX413703.1	GI:21446160				
Conservative	AX413703.1	AX413703.1	AX413703.1	AX413703.1	GI:21446160				
Mismatches	AX413703.1	AX413703.1	AX413703.1	AX413703.1	GI:21446160				
Indels	AX413703.1	AX413703.1	AX413703.1	AX413703.1	GI:21446160				
Gaps	AX413703.1	AX413703.1	AX413703.1	AX413703.1	GI:21446160				
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Db	AX413703.1	AX413703.1	AX413703.1	AX413703.1	GI:21446160				
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DEFINITION	AX415879	AX415879	AX415879	AX415879.1	GI:21448336				
ACCESSION	AX415879	AX415879	AX415879	AX415879.1	GI:21448336				
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KEYWORDS	AX415879.1	AX415879.1	AX415879.1	AX415879.1	GI:21448336				
SOURCE	AX415879.1	AX415879.1	AX415879.1	AX415879.1	GI:21448336				
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TITLE	AX415879.1	AX415879.1	AX415879.1	AX415879.1	GI:21448336				
JOURNAL	AX415879.1	AX415879.1	AX415879.1	AX415879.1	GI:21448336				
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ORIGIN	AX415879.1	AX415879.1	AX415879.1	AX415879.1	GI:21448336				
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Best Local Similarity	AX415879.1	AX415879.1	AX415879.1	AX415879.1	GI:21448336				
Matches	AX415879.1	AX415879.1	AX415879.1	AX415879.1	GI:21448336				
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Mismatches	AX415879.1	AX415879.1	AX415879.1	AX415879.1	GI:21448336				
Indels	AX415879.1	AX415879.1	AX415879.1	AX415879.1	GI:21448336				
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Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

REFERENCE

1 Kunst, F. and Glaser, P.
Listeria innocua, genome and applications
Patent: WO 0228891-A 2870 11-APR-2002;
INSTITUT PASTEUR (FR) ; CENTRE NATIONAL DE LA RECHERCHE
SCIENTIFIQUE (CNRS) (FR)

FEATURES

source
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Location/Qualifiers
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.8;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1447 TTACGGCTGGATTGCTGTG 1428

RESULT 3

AE017262_28/c

WPCOMMENT

Sequence split into 29 fragments LOCUS AE017262 Accession AE017262

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AE017262_02 200001 310000
AE017262_03 300001 410000
AE017262_04 400001 510000
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AE017262_27 2700001 2810000
AE017262_28 2800001 2905187

Continuation (29 of 29) of AE017262 from base 2800001 (AE017262 Listeria monocytogenes E

Query Match 100.0%; Score 20; DB 15; Length 105187;

Best Local Similarity 100.0%; Pred. No. 2.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 69060 TTACGGCTGGATTGCTGTG 69041

RESULT 4

AL591984/c

LOCUS

DEFINITION Listeria monocytogenes strain EGD, complete genome, segment 12/12.

ACCESSION AL591984 AL591824

VERSION

AL591984.1 GI:16412145

KEYWORDS

Listeria monocytogenes

SOURCE

Listeria monocytogenes

ORGANISM

Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

REFERENCE

AUTHORS

1 Glaser, P., Frangeul, L., Buchrieser, C., Rusniok, C., Amend, A.,
Baquero, F., Berche, P., Bloeker, H., Brandt, P., Chakraborty, T.,
Charbit, A., Chetouani, F., Couve, E., de Daruvar, A., Denoux, P.,
Domann, E., Dominguez-Bernal, G., Duchaud, E., Durant, L.,
Dussurget, O., Entian, K.D., Fsihi, H., Garcia-del Portillo, F.,
Garido, P., Gautier, L., Goebel, W., Gomez-Lopez, N., Hain, T.,
Hauf, J., Jackson, D., Jones, L.M., Kaerst, U., Kref, J., Kuhn, M.,
Kunst, F., Kurapat, G., Madueno, E., Maitournam, A., Vicente, J.M.,
Ng, E., Nedjari, H., Nordsiek, G., Novella, S., de Palos, B.,
Perez-Diaz, J.C., Purcell, R., Remmel, B., Rose, M., Schlueter, T.,
Simoes, N., Tierrez, A., Vazquez-Boland, J.A., Voss, H., Wehland, J. and
Cossart, P.

TITLE

Comparative genomics of Listeria species

JOURNAL

Science 294 (5543), 849-852 (2001)

PUBMED

11679669

REFERENCE

2 (bases 1 to 225528)

AUTHORS

Glaser, P., Frangeul, L. and Rusniok, C.

TITLE

Direct Submission

JOURNAL

Submitted (06-JUN-2001) Glaser P., Institut Pasteur, Genomique des

Microorganismes Pathogenes, 25 rue du Docteur Roux, 75724 Paris

COMMENT

Cedex 15, FRANCE

E-mail: pglaser@pasteur.fr

Phone: +33 1 45 68 89 96, Fax: +33 (0)1 45 68 87 86.

FEATURES

source

1. 225528
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Dehoux, P., Dusurget, O., Chetouani, F., Nedjari, H., Glaser, P., Kunst, F., Cosart, P., Daniels, J., Goebel, W., Kreft, J., Kuhn, M., Ng, E., Vasquez-Boland, J., Dominguez-Bernal, G., Garrido-Garcia, P., Tierrez-Martinez, A., Amend, A., Chakraborty, T., Domann, E., Hain, T., Berche, P., Charbit, A., Durand, L., Perez-Diaz, J. C., Baquero, F., Garcia del Portillo, F., Gomez-Lopez, N., Madueno, E., de Pablo, B., Wehland, J., Kaerst, U., Entian, K. D., Hauf, J., Rose, M. and Voss, H., *Listeria monocytogenes* genome, polypeptides and uses Patent: WO 01/118-A 2863 11-APR-2001; INSTITUT PASTEUR (FR)

TITLE

JOURNAL

FEATURES

source

Location/Qualifiers

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to 0.649.980 length: 349.980 <223>seq 2856 : From
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to 2.944.528 length: 244.528"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 208599 TTACGGCTGGATTGCTGTG 208580

RESULT 6
BX649277/c 125366 bp DNA linear VRT 23-OCT-2003
LOCUS
DEFINITION Zebrafish DNA sequence from clone DKEYP-67A10 in linkage group 20,
complete sequence.

ACCESSION BX649277
VERSION BX649277.5 GI:37936349
KEYWORDS HTG.

SOURCE Danio rerio (zebrafish)

ORGANISM

Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 125366)

AUTHORS Lovell, J.

Direct Submission

TITLE Submitted (22-OCT-2003) Wellcome Trust Sanger Institute, Hinxton,

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Oct 23, 2003 this sequence version replaced gi:37718596.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: zfish-help@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate

chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep Clone-derived zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhiyong Bao and Sean Eddy, submitted), and those beginning 'dr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see

http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml DKEYP-67A10 is from a zebrafish BAC library

VECTOR: pindigobAC-5.

FEATURES

source

Location/Qualifiers

1. 125366

/organism="Danio rerio"

/mol_type="genomic DNA"

/db_xref="taxon:7955"

/clones="DKEYP-67A10"

/clone_lib="DanioKeyPilot"

ORIGIN

Query Match 95.0%; Score 19; DB 11; Length 125366;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTACGGCTGGATTGCTGTG 19
|||||
Db 123540 TTACGGCTGGATTGCTGTG 123522

RESULT 7

LOCUS

DEFINITION BX649385 165089 bp DNA linear VRT 28-OCT-2003

complete sequence.

ACCESSION BX649385

VERSION BX649385.8 GI:38044030

KEYWORDS HTG.

SOURCE Danio rerio (zebrafish)

ORGANISM

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 165089)

AUTHORS Dyer, L.

Direct Submission

TITLE Submitted (28-OCT-2003) Wellcome Trust Sanger Institute, Hinxton,

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Oct 29, 2003 this sequence version replaced gi:37992151.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: zfish-help@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 14, 2006, 13:20:45 ; Search time 131.789 Seconds
(without alignments)
10189.779 Million cell updates/sec

Title: US-10-767-441-26

Perfect score: 21

Sequence: 1 tgtaaccgcgttacacagtt 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_env.*
2: gb_pat.*
3: gb_ph.*
4: gb_pl.*
5: gb_pr.*
6: gb_ro.*
7: gb_sts.*
8: gb_sy.*
9: gb_un.*
10: gb_vi.*
11: gb_ov.*
12: gb_htg.*
13: gb_in.*
14: gb_om.*
15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	759	2	AX415918 Sequence
2	21	100.0	2556	2	AX413703 Sequence
3	21	100.0	2556	2	AX415879 Sequence
4	21	100.0	105187	15	AE017262.28 Continuation (29 o
5	21	100.0	225528	15	AL591984 Listeria
6	21	100.0	244528	2	AX641673 Sequence
7	18.4	87.6	265444	12	AC132999 Rattus no
8	17.8	84.8	419	2	AR220914 Sequence
9	17.8	84.8	1310	5	BC05197 Homo sapi
10	17.8	84.8	2017	4	AK101759 Oryza sat
11	17.8	84.8	3084	2	AX416693 Sequence
12	17.8	84.8	110000	4	AP008207 322 Continuation (323
13	17.8	84.8	151085	4	AP003239 Oryza sat
14	17.8	84.8	209050	5	AC010733 Homo sapi
15	17.4	82.9	155656	5	AC019014 Homo sapi
16	17.4	82.9	186281	5	AC083874 Homo sapi
17	16.8	80.0	92466	5	AC092114 Homo sapi
18	16.8	80.0	106123	5	AL158015 Human DNA

Continuation (6 of
AL513483 Homo sapi
AC133546 Homo sapi
AC130700 Mus muscu
AC084705 Homo sapi
AC111127 Mus muscu
CT486009 Mus muscu
AC126023 Mus muscu
AC022068 Homo sapi
AC139867 Mus muscu
AC160493 Bos tauru
AC169595 Bos tauru
BD129605 Polynucle
X16619 Chlamydomon
AX695470 Sequence
AC174653 Strongylo
AL805916 Mouse DNA
AC010774 Homo sapi
AC008970 Homo sapi
AC146152 Pan trogl
AC091987 Homo sapi
AC092061 Homo sapi
AC073115 Homo sapi
AC072060 Homo sapi
AC073350 Homo sapi
AC092959 Homo sapi
AC112507 Homo sapi

ALIGNMENTS

RESULT 1
AX415918
LOCUS AX415918 759 bp DNA linear PAT 02-SEP-2002
DEFINITION Sequence 2909 from Patent WO0228891.
ACCESSION AX415918
VERSION AX415918.1 GI:21448375

KEYWORDS
SOURCE Listeria monocytogenes ATCC 19115

ORGANISM Listeria monocytogenes ATCC 19115

REFERENCE 1 Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

AUTHORS Kunst, F. and Glaser, P.

TITLE Listeria inocua, genome and applications

JOURNAL Patent: WO 0228891-A 2909 11-APR-2002;

INSTITUT PASTEUR (FR); CENTRE NATIONAL DE LA RECHERCHE

SCIENTIFIQUE (CNRS) (FR)

LOCATION/Qualifiers

1. .759

/organism="Listeria monocytogenes ATCC 19115"

/mol_type="unassigned DNA"

/db_xref="taxon:116281"

source

ORIGIN

Query Match 100.0%; Score 21; DB 2; Length 759;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACCCGCTTACACAGTT 21

|||||

Db 363 TGTAAACCCGCTTACACAGTT 383

RESULT 2

AX413703

LOCUS AX413703 2556 bp DNA linear PAT 02-SEP-2002

DEFINITION Sequence 694 from Patent WO0228891.

ACCESSION AX413703

VERSION AX413703.1 GI:21446160

KEYWORDS Listeria monocytogenes EGD-e

SOURCE Listeria monocytogenes EGD-e

ORGANISM Listeria monocytogenes EGD-e

Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

REFERENCE 1

AUTHORS Kunst, F. and Glaser, P.

TITLE Listeria innocua, genome and applications

JOURNAL Patent: WO 0228891-A 694 11-APR-2002;

INSTITUT PASTEUR (FR) ; CENTRE NATIONAL DE LA RECHERCHE

SCIENTIFIQUE (CNRS) (FR)

FEATURES Location/Qualifiers

source

1. .2556

/organism="Listeria monocytogenes EGD-e"

/mol_type="unassigned DNA"

/db_xref="taxon:169963"

ORIGIN

Query Match 100.0%; Score 21; DB 2; Length 2556;

Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACCCCGCTTACACAGTT 21

|||||

Db 837 TGTAAACCCCGCTTACACAGTT 857

RESULT 3

AX415879

LOCUS AX415879

DEFINITION Sequence 2870 from Patent WO0228891.

ACCESSION AX415879

VERSION AX415879.1 GI:21448336

KEYWORDS Listeria monocytogenes EGD-e

SOURCE Listeria monocytogenes EGD-e

ORGANISM Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

REFERENCE 1

AUTHORS Kunst, F. and Glaser, P.

TITLE Listeria innocua, genome and applications

JOURNAL Patent: WO 0228891-A 2870 11-APR-2002;

INSTITUT PASTEUR (FR) ; CENTRE NATIONAL DE LA RECHERCHE

SCIENTIFIQUE (CNRS) (FR)

FEATURES Location/Qualifiers

source

1. .2556

/organism="Listeria monocytogenes EGD-e"

/mol_type="unassigned DNA"

/db_xref="taxon:169963"

ORIGIN

Query Match 100.0%; Score 21; DB 2; Length 2556;

Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACCCCGCTTACACAGTT 21

|||||

Db 837 TGTAAACCCCGCTTACACAGTT 857

RESULT 4

AE017262.28

WPCOMMENT

Sequence split into 29 fragments LOCUS AE017262 Accession AE017262

Fragment Name

Begin End

AE017262_00 1 110000

AE017262_01 100001 210000

AE017262_02 200001 310000

AE017262_03 300001 410000

AE017262_04 400001 510000

AE017262_05 500001 610000

AE017262_06 600001 710000

AE017262_07 700001 810000

AE017262_08 800001 910000

AE017262_09 900001 1010000

AE017262_10 1000001 1110000

AE017262_11 1100001 1210000

AE017262_12 1200001 1310000

AE017262.13 1300001 1410000

AE017262_14 1400001 1510000

AE017262_15 1500001 1610000

AE017262_16 1600001 1710000

AE017262_17 1700001 1810000

AE017262_18 1800001 1910000

AE017262_19 1900001 2010000

AE017262_20 2000001 2110000

AE017262_21 2100001 2210000

AE017262_22 2200001 2310000

AE017262_23 2300001 2410000

AE017262_24 2400001 2510000

AE017262_25 2500001 2610000

AE017262_26 2600001 2710000

AE017262_27 2700001 2810000

AE017262_28 2800001 2905187

Continuation (29 of 29) of AE017262 from base 2800001 (AE017262 Listeria monocytogenes

Query Match 100.0%; Score 21; DB 15; Length 105187;

Best Local Similarity 100.0%; Pred. No. 1.8;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACCCCGCTTACACAGTT 21

|||||

Db 68450 TGTAAACCCCGCTTACACAGTT 68470

RESULT 5

AL591984

LOCUS AL591984

DEFINITION Listeria monocytogenes strain EGD, complete genome, segment 12/12.

ACCESSION AL591984 AL591824

VERSION AL591984.1 GI:16412145

KEYWORDS Listeria monocytogenes

SOURCE Listeria monocytogenes

ORGANISM Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

REFERENCE 1

AUTHORS Glaser, P., Frangeul, L., Buchrieser, C., Rusniok, C., Amend, A.,

Baguer, F., Berche, P., Bloeker, H., Brandt, P., Chakraborty, T.,

Charbit, A., Chetoui, F., Couve, E., de Daruvar, A., Dehoux, P.,

Domann, E., Dominguez-Bernal, G., Duchaud, E., Durant, L.,

Dussurget, O., Ertan, K. D., Fsihi, H., Garcia-del Portillo, P.,

Garrido, P., Gautier, L., Goebel, W., Gomez-Lopez, N., Hain, T.,

Haut, J., Jackson, D., Jones, L. M., Kaerst, U., Kretz, J., Kuhn, M.,

Kunst, F., Kurapkat, G., Madueno, E., Maitournam, A., Vicente, J. M.,

Ng, E., Nedjari, H., Nordstieck, G., Novella, S., de Pablo, B.,

Perez-Diaz, J. C., Purcell, R., Remmel, B., Rose, M., Schluter, T.,

Simoes, N., Tierrez, A., Vazquez-Boland, J. A., Voss, H., Wehland, J. and

Cossart, P.

TITLE Comparative genomics of Listeria species

JOURNAL Science 294 (5543), 849-852 (2001)

PUBMED 11679669

REFERENCE 2 (bases 1 to 225528)

AUTHORS Glaser, P., Frangeul, L. and Rusniok, C.

TITLE Direct Submission

JOURNAL Submitted (06-JUN-2001) Glaser P., Institut Pasteur, Genomique des

Microorganismes Pathogenes, 25 rue du Docteur Roux, 75724 Paris

Cedex 15, FRANCE

COMMENT E-mail: pglaser@pasteur.fr

Phone: +33 1 45 68 89 96. Fax: +33 (0)1 45 68 87 86.

FEATURES Location/Qualifiers

source

1. .225528

/organism="Listeria monocytogenes"

/mol_type="genomic DNA"

/strain="EGD-e"

/db_xref="taxon:1639"

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/transl_table=11

gene

CDS


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/db_xref="InterPro:IPR010763"
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/translation="MNKKFENLPKNNFALFLAKDKNSLEVVVAARGFAVPGIV
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AGTLNGLPETYNALVRPTGKIVGLSSGDEITAEBAVDYLSANIPSIKFMISIEG
TKYLDLVLTIAADKIGVIGEPAGGIGADNILEITTAIKSTGIPFYMPHIFGKTID
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NLDPTYHKQAKTGAFMSFDGAKIYAPESAKIAALYLVSEGFEDQLVSGDTRK
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TVLGLKILGASRLNDAAAEGLDLIVEKIITAEERLACVNFEDHRLNKDILLHLOP
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complement(6953..8211)
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